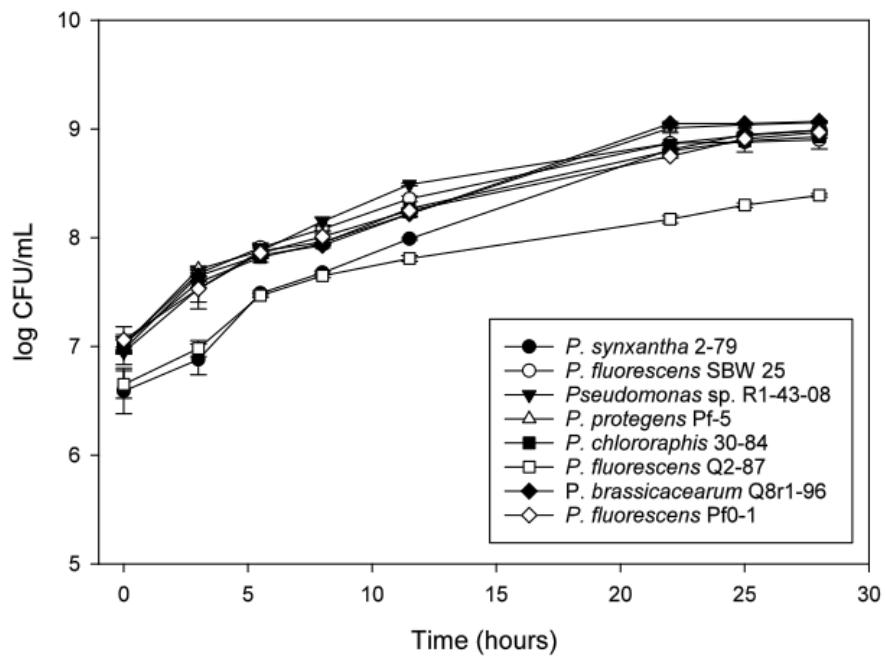
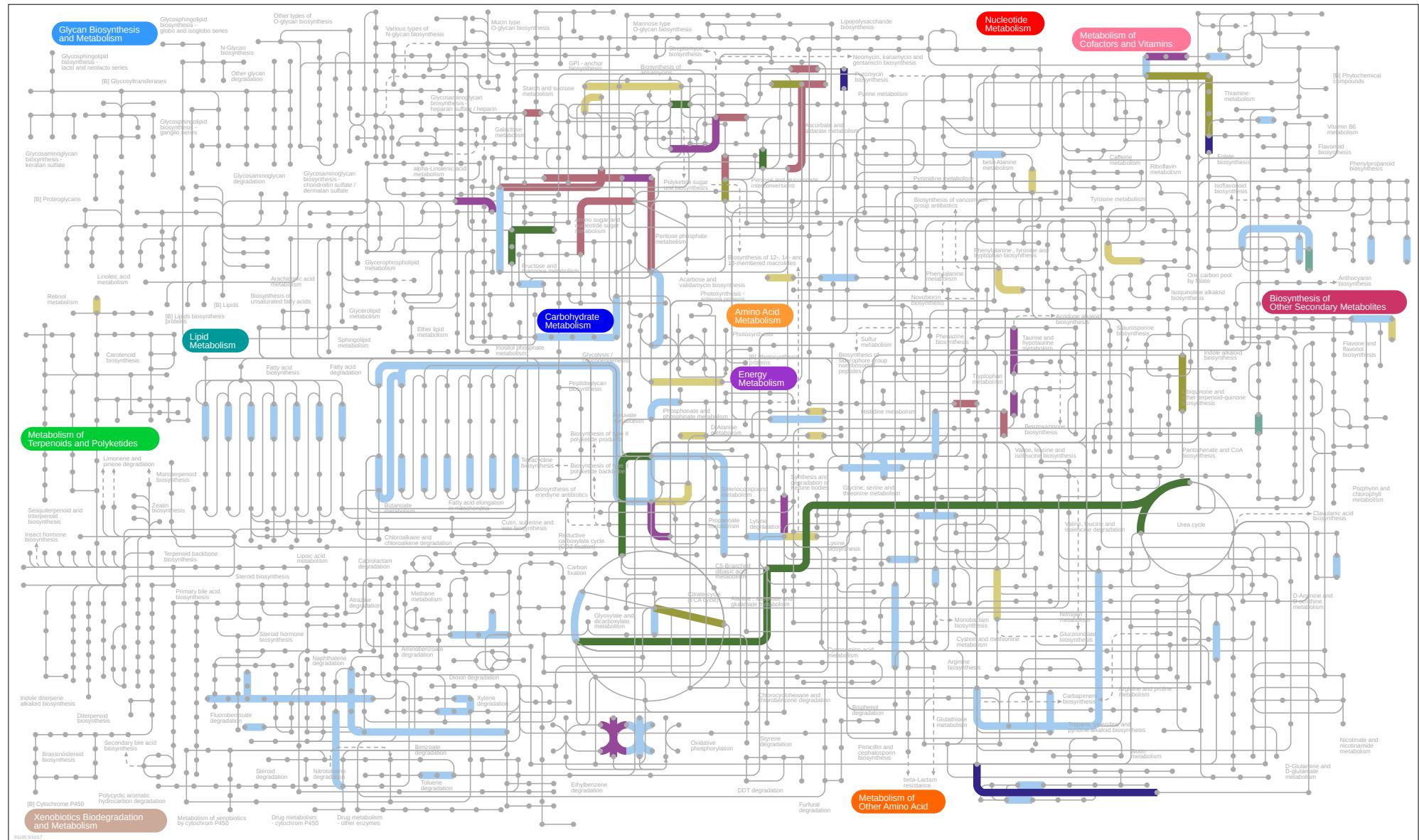


**Figure S1.** Mass chromatograms of root secretions and authentic standards showing the presence of glycine betaine (A), proline (B), and hydroxyectoine (C) in exudates of hydroponically grown *Brachypodium* plants. For each compound, panels on the left show selected ion chromatograms, while panels on the right depict accurate mass comparisons.



**Figure S2.** The growth of the studied *Pseudomonas* strains at 25°C in 21C medium amended with root exudates. To mimic rhizosphere conditions, the bacteria were grown statically at 72% air saturation.

### **Figure S3.** Metabolic map of upregulated pathways.



- *P. synxantha* 2-79

- *P. fluorescens* SBW25

- *Pseudomonas* sp. R1-43-08

- *P. brassicacearum* Q8r1-96

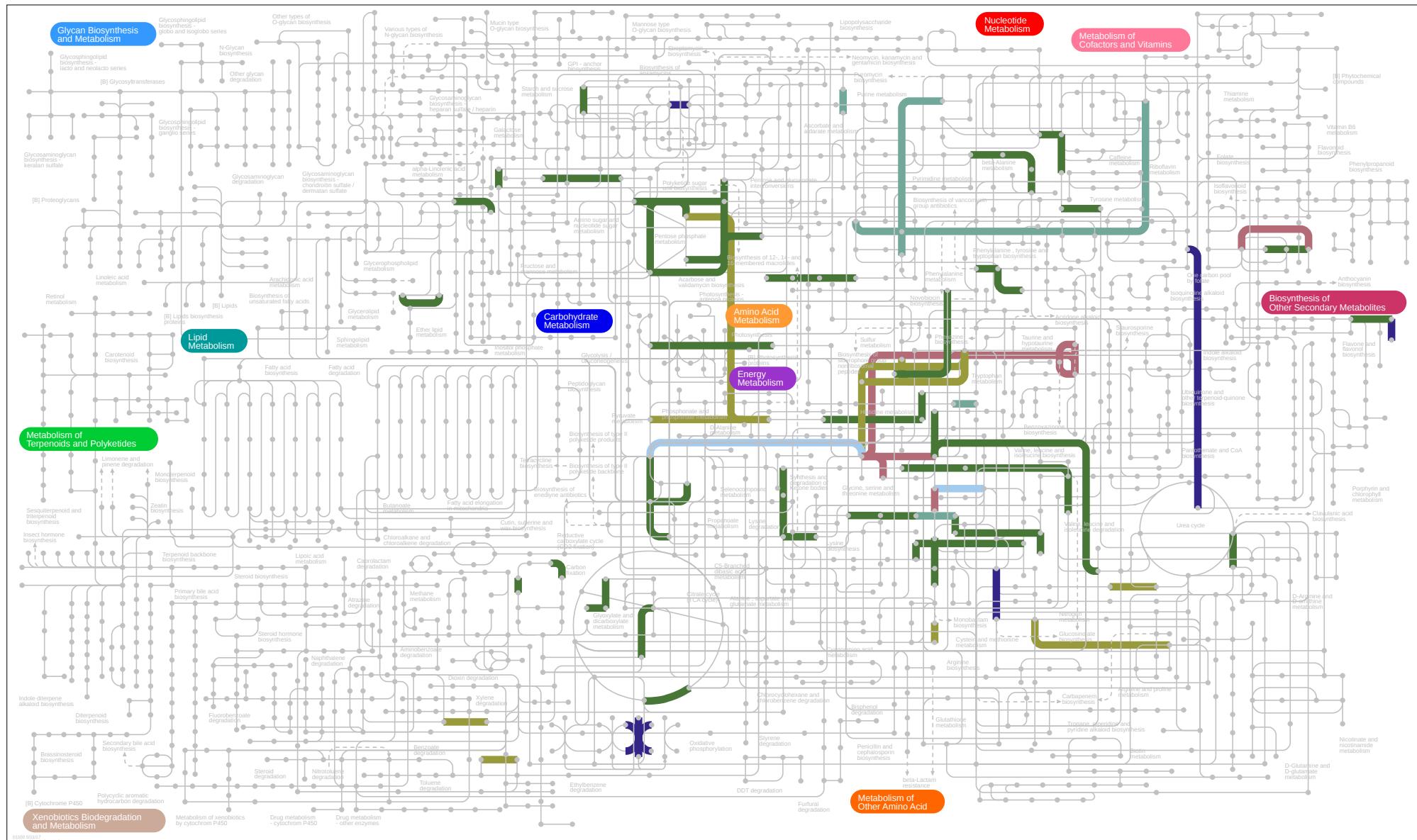
- *P. fluorescens* Q2-87

- *P. chlororaphis* 30-84

- *P. protegens* Pf-5

- *P. fluorescens* Pf0-1

**Figure S4. Metabolic map of downregulated pathways.**



- *P. synxantha* 2-79

- *P. fluorescens* SBW25

- *Pseudomonas* sp. R1-43-08

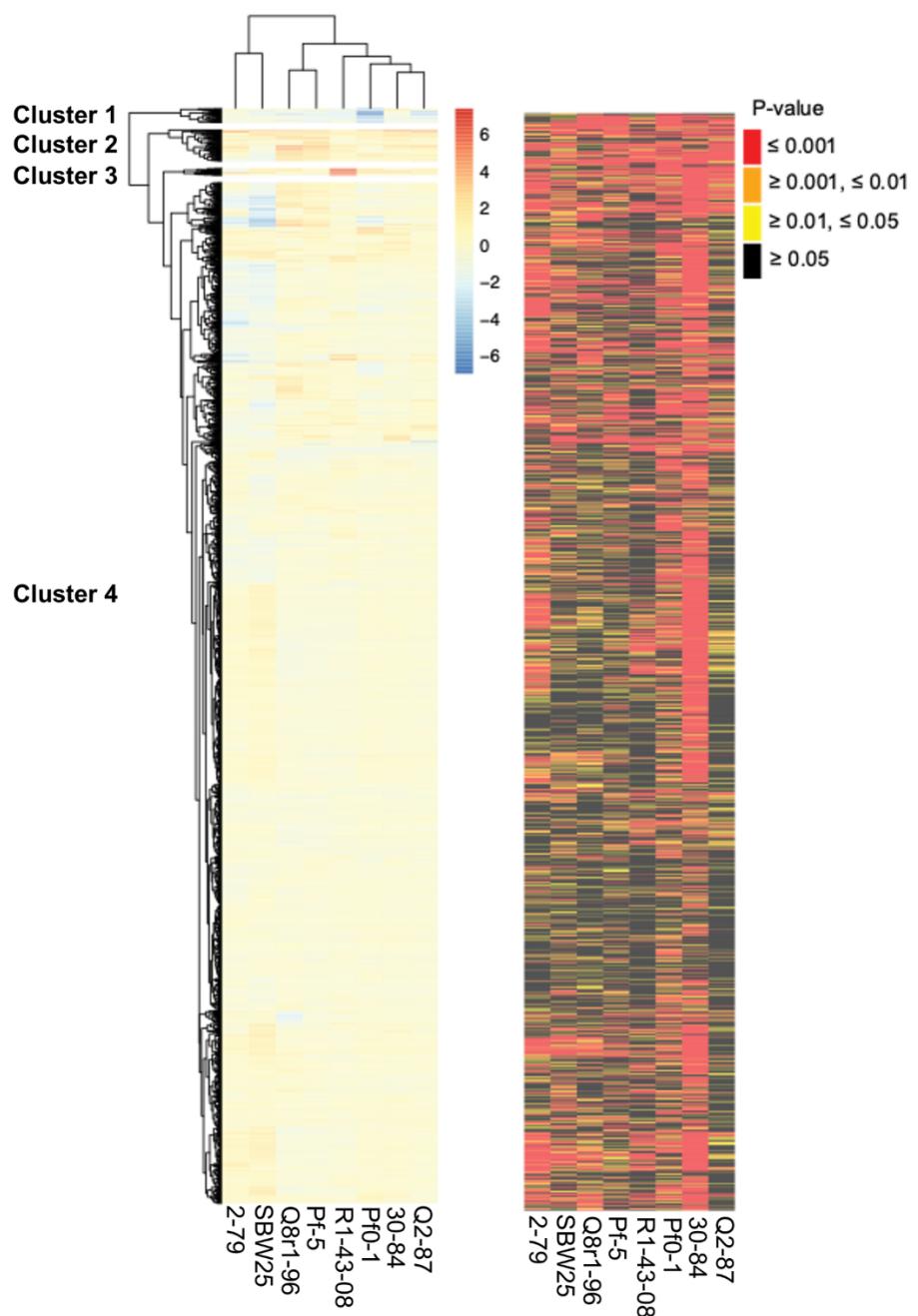
- *P. brassicacearum* Q8r1-96

- *P. fluorescens* Q2-87

- *P. chlororaphis* 30-84

- *P. protegens* Pf-5

- *P. fluorescens* Pf0-1



**Figure S5.** Hierarchical clustering heatmap for core *Pseudomonas* genes (left panel) constructed using Euclidean distance. The clustering was computed using the `hclust` function of the `pheatmap` R module (<https://CRAN.R-project.org/package=pheatmap>). Also shown is the heatmap of corresponding p-adj values (right panel). The corresponding numerical data are listed in supplemental table S13.